

Figure 1:

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AS 01: 3'-teg-G*G*G C*C*C*G G*C A*C*C G*T*C*C T*T*C*G
AS 02: 3'-teg-G*G*G*T*C A A G*C*C*C T*C*T G*T A*C*C*G
AS 03: 3'-teg-G*C*C*C T*C*T G*T A*C*C G*C*C*C G*C*A*A
AS 04: 3'-teg-T*A*C*C G*C*C*C G*C A A*T*T*T*C G A*G*A
AS 05: 3'-teg-T*T*C*G A G A*G*C A*C*C G*T A A*T A*G*G
AS 06: 3'-teg-G*A*A*T A*C G A*C*C*C*T A*C A*C G G*A*A
AS 07: 3'-teg-A*C*A*C G G A A*T*C*T C*C*T*A A*T A*C*C
AS 08: 3'-teg-C*T*C*C*T A A*T A*C*C G*C A A*A*T G*A*C
AS 09: 3'-teg-C*C*G*C*A A A*T G A*C*C*G G G A*A T*A*A
AS 10: 3'-teg-A*C*G G A*C A G*C*C*C T*T*G A*C*C G*T*A
AS 11: 3'-teg-G*G*A*C A G*C*C*C T*T*G A*C*C G*T A*T A*A*A
AS 12: 3'-teg-G*C*C*C T*T*G A*C*C G*T A*T A A*A G*A*A
AS 13: 3'-teg-G*G*A A*C*A*C A A*C*C*G T*C*C*G T*T*A*C
AS 14: 3'-teg-T*G*T A*C A*C G*T G*T A*C G*C*C G*T A*A
AS 15: 3'-teg-G*C*C*T C*C*T G*T C*C*A G*C*C*G C*C*A*A
AS 16: 3'-teg-G*G*A*C*C G A*C*A T*T*G C*A*C G*T C*T A*A*A

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*: Thioester

_: 2'-O-Methylation

teg: Triethylene glycol spacer

Figure 2

| | | | | | | |
|----------------|---|----|----|----|----|----|
| | 10 | 20 | 30 | 40 | 50 | 60 |
| | | | | | | |
| OB-RGRP_human | -----MAG-VKALVALSFSGAIGLTFMLMGCALP3YGVWPLFVLIFHAIS | | | | | |
| My47_human | -----MAG- IKALISLSFGGAIGLMFLMGCALPIYNKYWPLFVLFYILS | | | | | |
| yt02_C.elegans | MCCHIHQCFDCCSMKNTILAVAALAFAGVVGLTFLVLGCALPRYGTWTPMFVITFYVLS | | | | | |
| YJ14_Yeast | -----MMEFKVSPLTKIIISLSGFLALGFLLVILSCAL--FHNYYPFLDILIFLLA | | | | | |
| | . : : : * : . : * : : : * . * * : : * : * : . : . : | | | | | |
| Consensus | MCCHIHQCF2222MAG2IKALI2LSF4GAIGLTFMLMGCALP3YG4YWPLFV24FY4LS | | | | | |

| | | | | | | |
|----------------|---|----|----|-----|-----|-----|
| | 70 | 80 | 90 | 100 | 110 | 120 |
| | | | | | | |
| OB-RGRP_human | PIPHFIKR-----VTYDSDATSSACRELAYFFTTGIVVSAFGFPVILARVAVIKWGACG | | | | | |
| My47_human | PIPYCIARR-----LVDDTDAMSNACKELAIFFLTGIVVSAFGLPIVFARAHLEWGACA | | | | | |
| yt02_C.elegans | PVPLLIARR-----FQEDMTGTN-ACIELALFITTGIVISAFALPIVLAHAGTIAMSACF | | | | | |
| YJ14_Yeast | PIPNTIFNAGNKYHTSDFMSDSENTGQDLAHFLTGMVLTSGIALPVVIFYHCQLIGHLSCI | | | | | |
| | * : * * . : : * * * * : * * . : : * : : : * : * | | | | | |
| Consensus | PIP44IARRGNKYH44DDMDATSNAC4ELA4FLTTGIVVSAF2LP2V2A2A4LI4WGAC4 | | | | | |

| | | | |
|----------------|-----------------------------------|-----|-----|
| | 130 | 140 | 150 |
| | | | |
| OB-RGRP_human | LVLAGNAVIFLTIQGFFLIFGRGDDFSWEQW- | | |
| My47_human | LVLTGNTVIFATILGFFLVFGSKDDFSWQQW- | | |
| yt02_C.elegans | LIFIANSEINFSVIIFYFRIFNGEDMNGMSLW- | | |
| YJ14_Yeast | MCMIGGLIIYSSIVIFKWFPPKDFNEDDSLFG | | |
| | : : . . : : * : . * | | |
| Consensus | LVLIGN42IFSTI4GFFLIFG44DDFSWS2WG | | |

Figure 3A

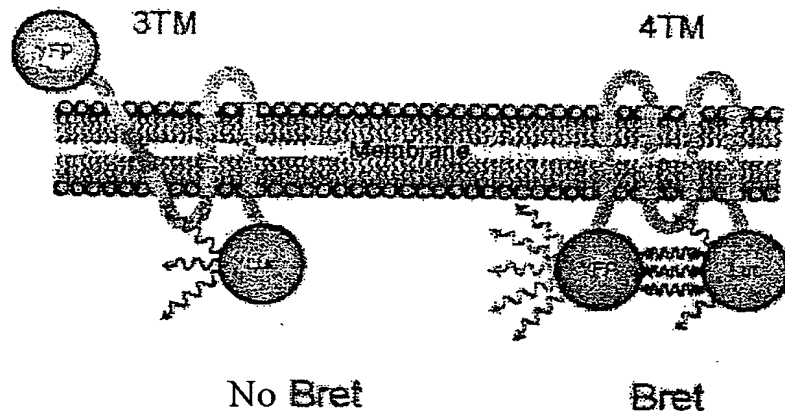


Figure 3B

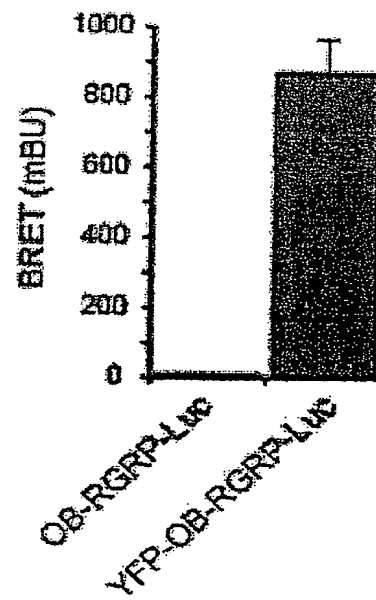


Figure 4 A

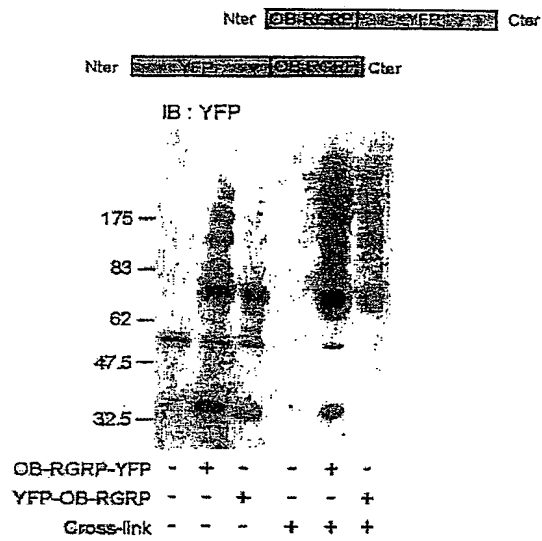


Figure 4B

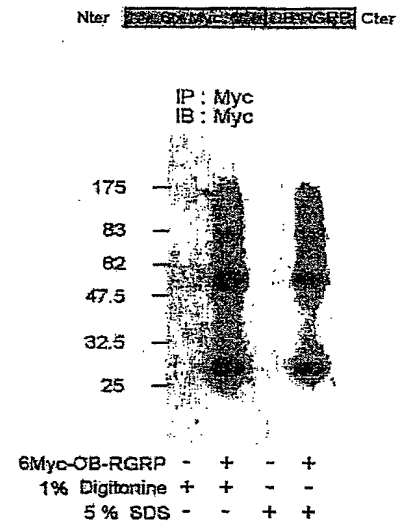


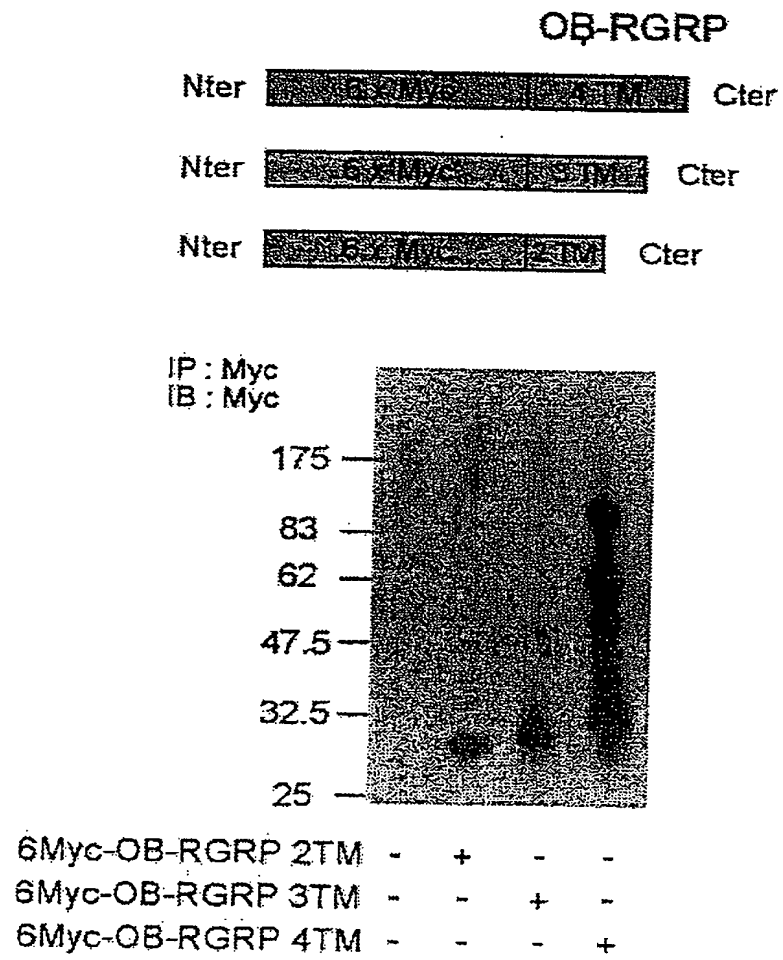
Figure 5

Figure 6 A

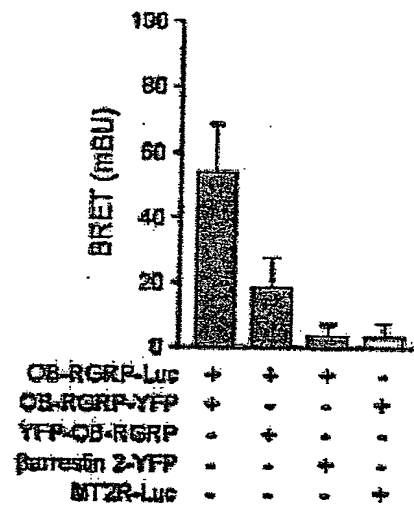


Figure 6B

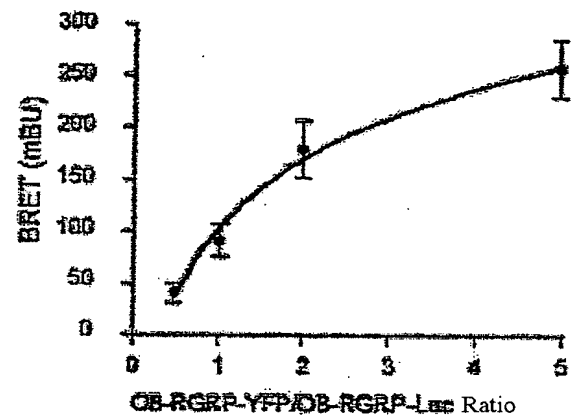


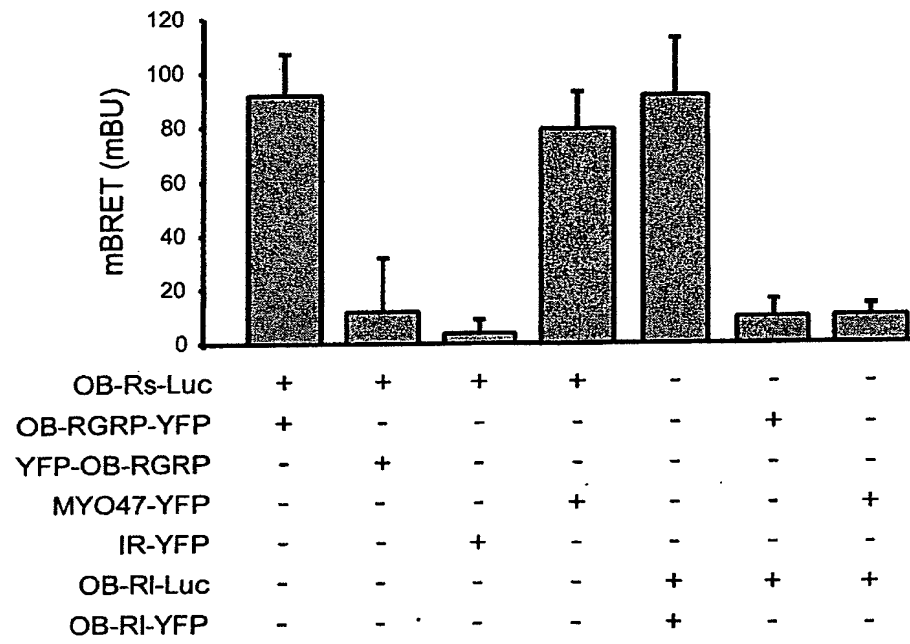
Figure 7

Figure 8a

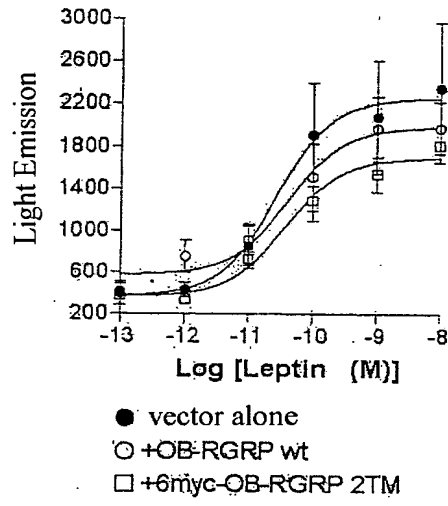


Figure 8b

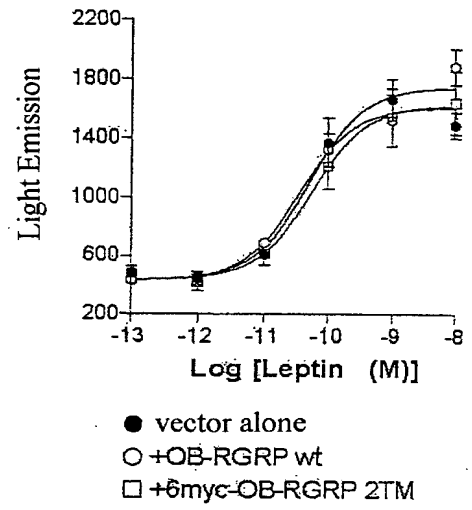


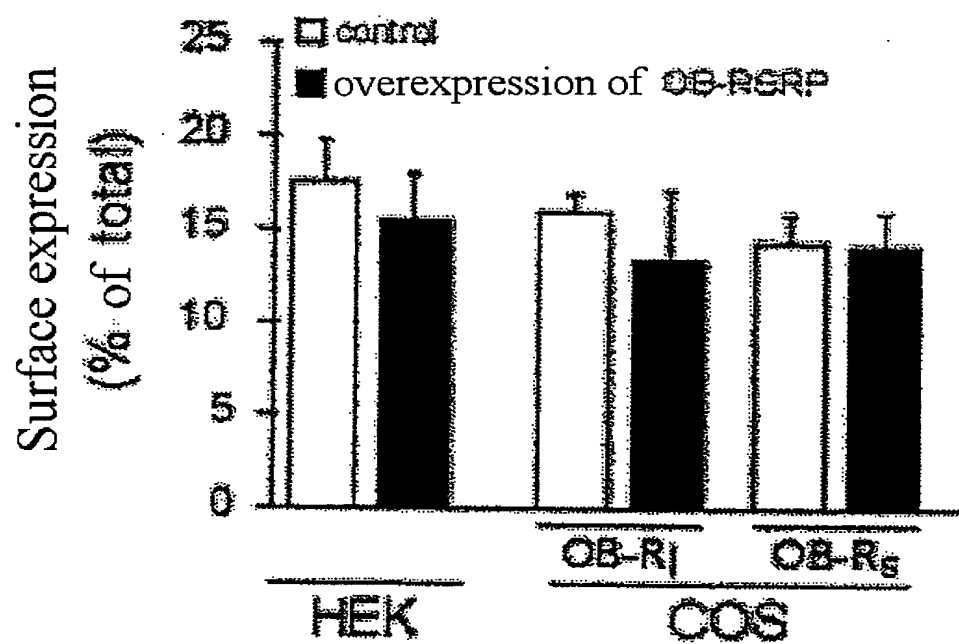
Figure 9

Figure 10a

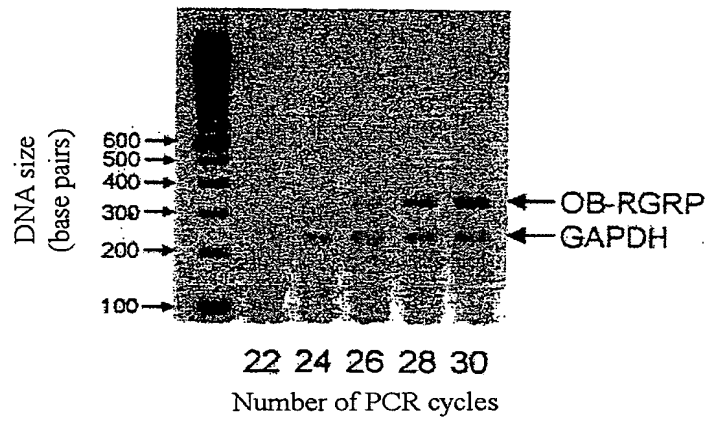


Figure 10b

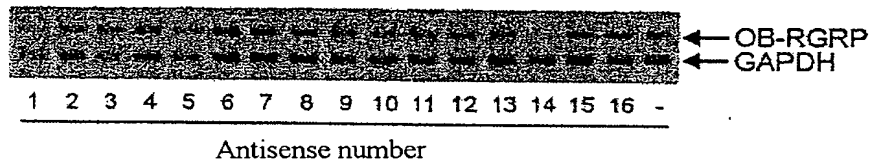
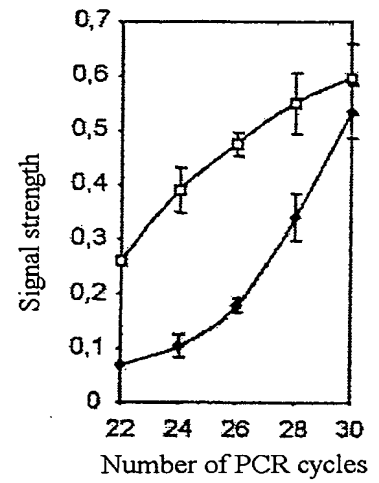


Figure 10c

FIGURE 11A

5' - gugccugucgggaacuggcTT -3'
 3' - TTcacggacagcccuugaccg -5'

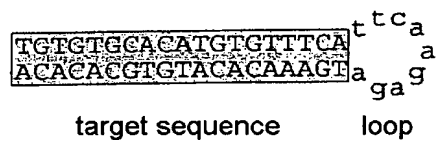


FIGURE 11C

FIGURE 11B

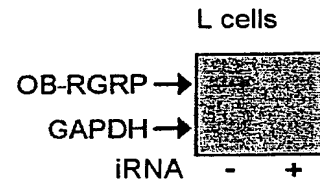
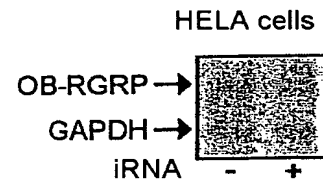


FIGURE 11D

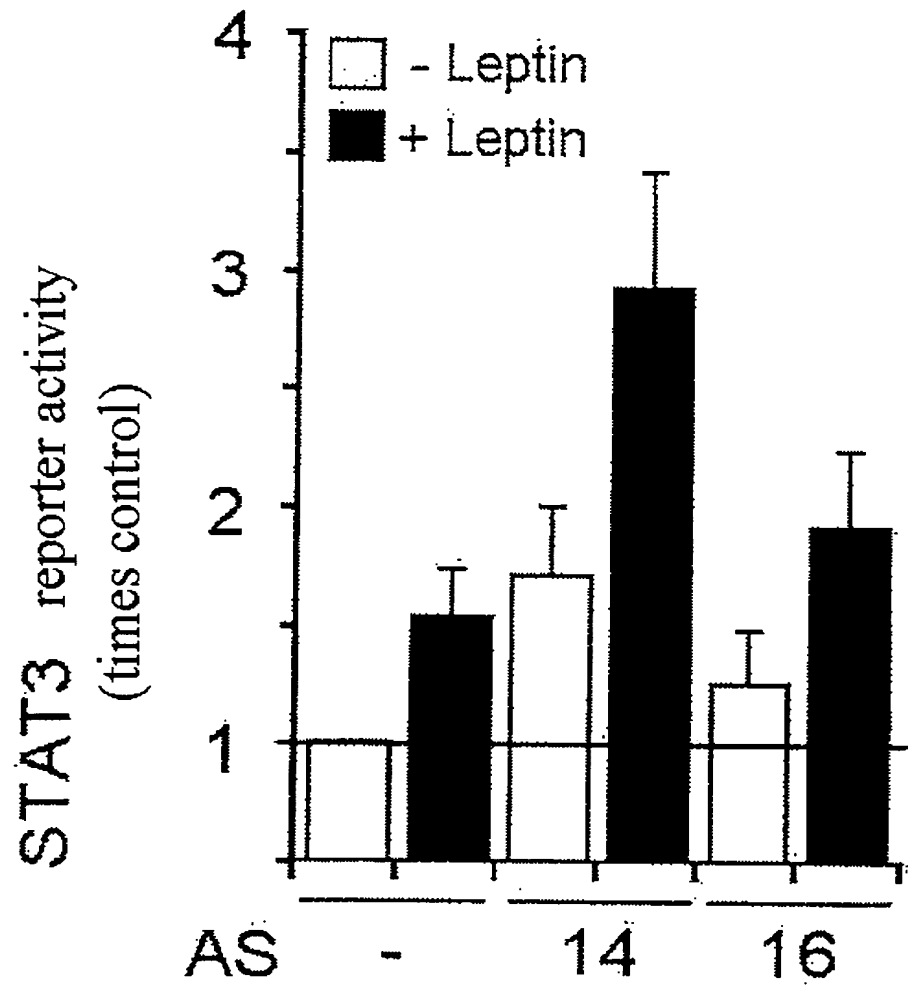
Figure 12

Figure 13